



SEQUENCE LISTING

<110> NAGY et al.
<120> HUMAN POLYPEPTIDES CAUSING OR LEADING TO THE KILLING
OF CELLS INCLUDING LYMPHOID TUMOR CELLS
<130> GPCG-P01-003
<140> 10/001934
<141> 2001-11-15
<150> PCT/US01/15625
<151> 2001-05-14
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<170> PatentIn version 3.0
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<223> "Xaa" represents any amino acid residue

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gagacgaaaa acatattctc aataaacctt ttagggaaat aggccagggt ttcaccgtaa	3540
cacgccacat cttgcgaata tatgtgtaga aactgccgga aatcgtcgtg gtattcactc	3600

cagagc gatg aaaacgtttc agtttgctca tggaaaacgg tgtaacaagg gtgaacacta 3660
 tcccatatca ccagctcacc gtctttcatt gccatacggg actccgggtg agcattcatc 3720
 aggcgggcaa gaatgtgaat aaaggccgga taaaacttgt gcttattttt ctttacggtc 3780
 tttaaaaagg ccgtaatatc cagctgaacg gtctgggttat aggtacattg agcaactgac 3840
 tgaaatgcct caaaatgttc tttacgatgc cattgggata tatcaacggg ggtatatcca 3900
 gtgatttttt tctccatttt agcttcctta gctcctgaaa atctcgataa ctcaaaaaat 3960
 acgcccggta gtgatcttat ttcattatgg tgaaagttgg aacctcaccg gacgtctaata 4020
 gtgagtttagc tcaactcatta ggcaccccag gctttacact ttatgcttcc ggctcgtatg 4080
 ttgtgtggaa ttgtgagcgg ataacaattt cacacaggaa acagctatga ccatgattac 4140
 gaatt 4145

<210> 73
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC1-VH
 <222> (1)..(120)

<400> 73

Gln	Val	Gln	Leu	Lys	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln	1	5	10	15
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser	20	25	30	
Gly	Val	Gly	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu	35	40	45	
Trp	Leu	Ala	Leu	Ile	Asp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Ser	Thr	Ser	50	55	60	
Leu	Lys	Thr	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	65	70	75	80
Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr	85	90	95	
Cys	Ala	Arg	Gln	Tyr	Gly	His	Arg	Gly	Gly	Phe	Asp	His	Trp	Gly	Gln	100	105	110	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	115	120										

<210> 74
 <211> 109
 <212> PRT

<213> artificial sequence

<220>

<221> MS-GPC1-VL

<222> (1)..(109)

<400> 74

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asn Glu
85 90 95

Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 75

<211> 118

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC6-VH

<222> (1)..(118)

<400> 75

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Gly Arg Tyr Ser Pro Asp Leu Trp Gly Gln Gly Thr

100	105	110
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Leu Val Thr Val Ser Ser
 115

<210> 76
 <211> 110
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC6-VL
 <222> (1)..(110)

<400> 76

Asp	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	

Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Gln	Ser	Val	Ser	Ser	Ser
			20					25					30		

Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
	35						40					45			

Ile	Tyr	Gly	Ala	Ser	Ser	Arg	Ala	Thr	Gly	Val	Pro	Ala	Arg	Phe	Ser
	50					55					60				

Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu
65					70					75				80	

Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Asn	Leu	Pro
				85					90					95	

Phe	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr		
			100					105					110		

<210> 77
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC8-VH
 <222> (1)..(120)

<400> 77

Gln	Val	Gln	Leu	Lys	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln
1				5					10					15	

Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		

Gly	Val	Gly	Val	Gly	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
	35						40					45			

Trp	Leu	Ala	Leu	Ile	Asp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Ser	Thr	Ser
	50					55					60				

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 78
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-VL
<222> (1)..(109)

<400> 78

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Pro Gln
85 90 95

Ala Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 79
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC10-VH
<222> (1)..(120)

<400> 79

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser

	20		25		30
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu					
	35		40		45
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser					
	50		55		60
Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val					
	65		70		75
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr					
		85		90	95
Cys Ala Arg Gln Leu His Tyr Arg Gly Gly Phe Asp Leu Trp Gly Gln					
	100		105		110
Gly Thr Leu Val Thr Val Ser Ser					
	115		120		

<210> 80
 <211> 109
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC10-VL
 <222> (1)..(109)

<400> 80

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln					
1		5		10	15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn					
	20		25		30
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu					
	35		40		45
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser					
	50		55		60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln					
	65		70		75
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Thr Met					
		85		90	95
Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly					
	100		105		

<210> 81
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>

<221> MS-GPC8-6-VH

<222> (1)..(120)

<400> 81

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 82

<211> 109

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC8-6-VL

<222> (1)..(109)

<400> 82

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
85 90 95

Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 83
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-10-VH
<222> (1)..(121)

<400> 83

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 84
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-10-VL
<222> (1)..(109)

<400> 84

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg
85 90 95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 85
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-17-VH
<222> (1)..(120)

<400> 85
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 86
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-17-VL
<222> (1)..(109)

<400> 86

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ser Val
 85 90 95
 Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

<210> 87
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC8-27-VH
 <222> (1)..(120)

<400> 87
 Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15
 Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30
 Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
 35 40 45
 Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
 50 55 60
 Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 88

<211> 115
<212> PRT
<213> artificial sequence

<220>

<221> MS-GPC8-27-VL

<222> (1)..(115)

<400> 88

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu
65 70 75 80

Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn
85 90 95

Val His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 110 115

<210> 89

<211> 120

<212> PRT

<213> artificial sequence

<220>

<221> MS-GPC8-6-13-VH

<222> (1)..(120)

<400> 89

Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 90
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-6-13-VL
<222> (1)..(109)

<400> 90
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Ala Asn
20 25 30
Tyr Val Thr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Asp His
85 90 95
Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 91
<211> 120
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-10-57-VH
<222> (1)..(120)

<400> 91
Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
1 5 10 15
Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30
Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45
Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80
 Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
 85 90 95
 Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 92
 <211> 109
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC8-10-57-VL
 <222> (1)..(109)

<400> 92
 Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
 20 25 30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ile Arg
 85 90 95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105

<210> 93
 <211> 120
 <212> PRT
 <213> artificial sequence

<220>
 <221> MS-GPC8-27-41-VH
 <222> (1)..(120)

<400> 93
 Gln Val Gln Leu Lys Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Pro Arg Tyr Arg Gly Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 94
<211> 109
<212> PRT
<213> artificial sequence

<220>
<221> MS-GPC8-27-41-VL
<222> (1)..(108)

<400> 94
Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
1 5 10 15

Arg Val Thr Ile Ser Cys Ser Gly Ser Glu Ser Asn Ile Gly Asn Asn
20 25 30

Tyr Val Gln Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Asn Val
85 90 95

His Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

1